

4518-0111PUS1.ST25.txt
SEQUENCE LISTING

<110> Igeneon Krebs-Immuntherapie Forschungs- & Entwickl

<120> Immunogenic Recombinant Antibody

<130> Immunogenic Recombinant AB

<140>

<141>

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 3973

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB 17-1A

<400> 1

```
ataggctagc ctcgagccac caccatgcat cagaccagca tgggcatcaa gatggaatca 60
cagactctgg tcttcatatc catactgctc tggttatatg gagctgatgg gaacattgta 120
atgacccaat ctcccaaate catgtccatg tcagtaggag agaggggtcac cttgacctgc 180
aaggccagtg agaatgtggt tacttatgtt tcntgggtatc aacagaaacc agagcagtct 240
cctaaactgc tgatatatgg ggcacccaac cggtagactg ggggtccnga tcgcttcaca 300
ggcagtggat ctgcaacaga tttcactctg accatcagca gtgtgcaggc tgaagacctt 360
gcagattatc actgtggaca ggggttacagc tatccgtaca cggttcggagg ggggaccaag 420
ctggaaataa aacgggctga tgctgcacca actgtatcca tcttcccacc atccagttag 480
cagttaacat ctggaggtgc ctcagtcgtg tgcttcttga acaacttcta ccccaaagac 540
atcaatgtca agtggaagat tgatggcagt gaacgacaaa atggcgctcct gaacagttgg 600
actgatcagg acagcaaaga cagcacctac agcatgagca gcacctcac gttgaccaag 660
gacgagtatg aacgacataa cagctatacc tgtgaggcca ctcacaagac atcaacttca 720
cccattgtca agagcttcaa caggaatgag tgtagacgc gtggatccgc ccctctccct 780
ccccccccc taacgttact ggccgaagcc gcttggaata aggccggtgt gcgtttgtct 840
atatgtgatt ttccaccata ttgccgtctt ttggcaatgt gagggcccgg aaacctggcc 900
ctgtcttctt gacgagcatt cctaggggtc tttcccctct cgccaaagga atgcaaggct 960
tgttgaatgt cgtgaaggaa gcagttcctc tggaagcttc ttgaagacaa acaacgtctg 1020
tagcgaccct ttgcaggcag cggaaccccc cacctggcga caggtgcctc tgcggccaaa 1080
agccacgtgt ataagataca cctgcaaagg cggcacaacc ccagtgccac gttgtgagtt 1140
ggatagttgt ggaaagagtc aaatggctct cctcaagcgt attcaacaag gggctgaagg 1200
atgcccagaa ggtaccccat tgtatgggat ctgatctggg gcctcgggtg acatgcttta 1260
catgtgttta gtcgaggtta aaaaaacgtc taggcccccc gaaccacggg gacgtggttt 1320
tcctttgaaa aacacgatga taatatggcc accaccatgg aatggagcag agtctttatc 1380
tttctcctat cagtaactgc aggtgttcac tcccagggtc agttgcagca gtctggagct 1440
gagctggtaa ggcctgggac ttcagtgaag gtgtcctgca aggcttctgg atacgccttc 1500
actaattact tgatagagtg ggtaaagcag aggcctggac agggccttga gtggattggg 1560
gtgattaatc ctggaagtgg tggtaactaa tacaatgaga agttcaaggg caaggcaaca 1620
ctgactgcag acaaatcctc cagcactgcc tacatgcagc tcagcagcct gacatctgat 1680
gactctgcgg tctatttctg tgcaagagat ggtccctggg ttgcttactg gggccaaggg 1740
actctggtea ctgtctctgc agccaaaaca acagcccat cggtctatcc actggcccct 1800
gtgtgtggag atacaactgg ctctcgggtg actctaggat gcctgggtcaa gggttatttc 1860
cctgagccag tgaccttgac ctggaactct ggatccctgt ccagtgggtg gcacaccttc 1920
ccagctgtcc tgcagtctga cctctacacc ctcagcagct cagtgactgt aacctcgagc 1980
acctggccca gccagtcctc cacctgcaat gtggcccacc cggcaagcag caccaagggtg 2040
gacaagaaaa ttgagcccgagg agggcccaca atcaagccct gtcctccatg caaatgcccc 2100
```

4518-0111PUS1.ST25.txt

```

gcacctaacc tcttgggtgg accatccgtc ttcattcttc ctccaaagat caaggatgta 2160
ctcatgatct ccctgagccc catagtcaca tgtgtggtgg tggatgtgag cgaggatgac 2220
ccagatgtcc agatcagctg gtttgtgaac aacgtggaag tacacacagc tcagacacaa 2280
acccatagag aggattacaa cagtactctc cgggtggtca gtgccctccc catccagcac 2340
caggactgga tgagtggcaa ggagttcaaa tgcaaggtca acaacaaaga cctcccagcg 2400
cccatcgaga gaacctctc aaaacccaaa gggtcagtaa gagctccaca ggtatatgtc 2460
ttgcctccac cagaagaaga gatgactaag aaacaggtca ctctgacctg catggtcaca 2520
gacttcatgc ctgaagacat ttacgtggag tggaccaaca acgggaaaac agagctaaac 2580
tacaagaaca ctgaaccagt cctggactct gatggttctt acttcatgta cagcaagctg 2640
agagtggaaa agaagaactg ggtggaaaga aatagctact cctgttcagt ggtccacgag 2700
ggtctgcaca atcaccacac gactaagagc ttctcccgga ctccgggtaa atgagtcgac 2760
acgcgtcgag catgcatcta gggcggccaa ttccgccccct ctccctcccc cccccctaac 2820
gttactggcc gaagccgctt ggaataaggc cgggtgtgct ttgtctatat gtgattttcc 2880
accatattgc cgtcttttgg caatgtgagg gcccggaac ctggccctgt cttcttgacg 2940
agcattccta ggggtctttc ccctctcgcc aaaggaatgc aaggctctgtt gaatgtcgtg 3000
aaggaagcag ttctctgga agcttcttga agacaaacaa cgtctgtagc gaccctttgc 3060
aggcagcgga accccccacc tggcgacagg tgcctctgcg gccaaaagcc acgtgtataa 3120
gatacacctg caaaggcggc acaaccccag tgccacgttg tgagttggat agttgtggaa 3180
agagtcaaat ggctctctc aagcgtattc aacaaggggc tgaaggatgc ccagaaggta 3240
ccccattgta tgggatctga tctggggcct cgggtgcacat gctttacatg tgtttagtcg 3300
aggttaaaaa aacgtctagg cccccgaac cacggggacg tggttttcct ttgaaaaaca 3360
cgatgataag cttgccacaa cccgggatcc tctagaccac catggttcga ccattgaact 3420
gcatcgtcgc cgtgtcccaa gatatgggga ttggcaagaa cggagaccta ccctggcctc 3480
cgctcaggaa cgagttcaag tacttccaaa gaatgaccac aacctcttca gtggaaggta 3540
aacagaatct ggtgattatg ggtaggaaaa cctggttctc cattcctgag aagaatcgac 3600
ctttaaagga cagaattaat atagttctca gtagagaact caaagaacca ccacgaggag 3660
ctcattttct tgccaaaagt ttggatgatg ctttaagact tattgaacaa ccggaattgg 3720
caagtaaagt agacatgggt tggatagtcg gaggcagttc tgtttaccag gaagccatga 3780
atcaaccagg ccacctcaga ctctttgtga caaggatcat gcaggaattt gaaagtgaca 3840
cgtttttccc agaaattgat ttggggaaat ataaacttct ccagaatac ccaggcgtcc 3900
tctctgaggt ccaggaggaa aaaggcatca agtataagtt tgaagtctac gagaagaaag 3960
actaagcggc cgc

```

<210> 2

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB 17-1A

<400> 2

```

Met Glu Trp Ser Arg Val Phe Ile Phe Leu Leu Ser Val Thr Ala Gly
 1              5              10              15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
          20              25              30

Pro Gly Thr Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe
          35              40              45

Thr Asn Tyr Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
          50              55              60

Glu Trp Ile Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn
          65              70              75              80

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
          85              90              95

```

4518-0111PUS1.ST25.txt

Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	Ser	Ala	Val
			100					105					110		
Tyr	Phe	Cys	Ala	Arg	Asp	Gly	Pro	Trp	Phe	Ala	Tyr	Trp	Gly	Gln	Gly
		115					120					125			
Thr	Leu	Val	Thr	Val	Ser	Ala	Ala	Lys	Thr	Thr	Ala	Pro	Ser	Val	Tyr
	130					135					140				
Pro	Leu	Ala	Pro	Val	Cys	Gly	Asp	Thr	Thr	Gly	Ser	Ser	Val	Thr	Leu
145					150					155					160
Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Leu	Thr	Trp
				165					170					175	
Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
			180					185					190		
Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	Thr	Ser	Ser
		195					200					205			
Thr	Trp	Pro	Ser	Gln	Ser	Ile	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser
	210					215					220				
Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys
225					230					235					240
Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro
				245					250					255	
Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser
			260					265					270		
Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp
		275					280					285			
Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr
	290					295					300				
Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val
305					310					315					320
Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu
				325					330					335	
Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg
			340					345					350		
Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val
		355					360					365			
Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr
	370					375					380				
Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr
385					390					395					400
Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu

405

410

415

Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
 420 425 430

Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
 435 440 445

Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
 450 455 460

Lys
 465

<210> 3

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB 17-1A

<400> 3

Met His Gln Thr Ser Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val
 1 5 10 15

Phe Ile Ser Ile Leu Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val
 20 25 30

Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val
 35 40 45

Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp
 50 55 60

Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala
 65 70 75 80

Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 85 90 95

Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 100 105 110

Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly
 115 120 125

Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val
 130 135 140

Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser
 145 150 155 160

Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys
 165 170 175

Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp
 180 185 190

4518-0111PUS1.ST25.txt

Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu
195 200 205

Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu
210 215 220

Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg
225 230 235 240

Asn Glu Cys

<210> 4
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mAB 17-1A

<400> 4
Met His Gln Thr Ser Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val
1 5 10 15

Phe Ile Ser Ile Leu Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val
20 25 30

Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val
35 40 45

Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp
50 55 60

Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala
65 70 75 80

Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
85 90 95

Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
100 105 110

Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly
115 120 125

Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala Pro Thr Val
130 135 140

Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser
145 150 155 160

Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys
165 170 175

Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp
180 185 190

Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu
 195 200 205

Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu
 210 215 220

Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg
 225 230 235 240

Asn Glu Cys

<210> 5

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB 17-1A

<400> 5

Met His Gln Thr Ser Met Gly Ile Arg Met Glu Ser Gln Thr Leu Val
 1 5 10 15

Phe Ile Ser Ile Leu Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val
 20 25 30

Met Thr Gln Ser Pro Arg Ser Met Ser Met Ser Val Gly Glu Arg Val
 35 40 45

Thr Leu Thr Cys Arg Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp
 50 55 60

Tyr Gln Gln Arg Pro Glu Gln Ser Pro Arg Leu Leu Ile Tyr Gly Ala
 65 70 75 80

Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 85 90 95

Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 100 105 110

Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly
 115 120 125

Gly Gly Thr Arg Leu Glu Ile Arg Arg Ala Asp Ala Ala Pro Thr Val
 130 135 140

Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser
 145 150 155 160

Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys
 165 170 175

Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp
 180 185 190

Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu

195

200

205

Thr	Leu	Thr	Lys	Asp	Glu	Tyr	Glu	Arg	His	Asn	Ser	Tyr	Thr	Cys	Glu
210						215					220				

Ala	Thr	His	Lys	Thr	Ser	Thr	Ser	Pro	Ile	Val	Lys	Ser	Phe	Asn	Arg
225					230					235					240

Asn Glu Cys